

RESULT 6								
Q6WH41	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	05-JUL-2004 (TREMBLrel. 27, Created)							
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)							
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)							
DE	Envelope glycoprotein (Fragment).							
GN	Name=env;							
	Human immunodeficiency virus 1.							
	Viruses; Retroviridae; Lentivirus.							
OX	NCBI_TaxID:11676;							
RN	SEQUENCE FROM N.A.							
RX	PubMed:14715797;							
RA	Pires I.L., Soares M.A., Speranza F.A.B., Ishii S.K., Vieira M.C.G.,							
RA	Gouveia M.I.P.S., Guimaraes M.A.A.M., De Oliveira F.E.,							
RA	Magnanini M.M.F., Brindeiro R.M., Tanuri A.;							
RT	"Prevalence of human immunodeficiency virus drug resistance mutations and subtypes in drug-naïve, infected individuals in the army health service of Rio de Janeiro, Brazil."							
RT	J. Clin. Microbiol. 42:426-430(2004).							
RL	EMBL; AY289055; AA068118; 1.							
DR	GO; GO:0016021; C:integral to membrane; IEA.							
DR	GO; GO:0019028; C:viral capsid; IEA.							
DR	GO; GO:0019031; C:viral envelope; IEA.							
DR	GO; GO:0005198; P:structural molecule activity; IEA.							
DR	InterPro; IPR00328; Env_GP41.							
DR	PFam; PF00517; GP41; 1.							
KW	Coat protein; Envelope protein; Glycoprotein; Transmembrane.							
FT	NON_TER 122 AA;							
FT	NON_TER 122 AA;							
SQ	SEQUENCE 122 AA; 14817 MW; PFE95657A2C81ACC CRC64;							
Q9EA97	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAR-2001 (TREMBLrel. 16, Created)							
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)							
Q9EA97	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9EA97	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 7								
Q7ZJR4	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-JUN-2003 (TREMBLrel. 24, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)							
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)							
DE	Envelope glycoprotein (Fragment).							
GN	Name=env;							
	Human immunodeficiency virus 1.							
	Viruses; Retroviridae; Lentivirus.							
OX	NCBI_TaxID:11676;							
RN	SEQUENCE FROM N.A.							
RX	PubMed:2280244; Published=12921095; DOI=10.1089/088922203322231003;							
RA	Swanson P.A., Devare S.G., Hackett J.R., Jr.;							
RT	"Molecular Characterization of 39 HIV-1 Isolates Representing Group M (Subtypes A-G) and Group O: Sequence Analysis of gag p24, pol							
RT	integrase, and env gp41."							
RL	AIDS Res. Hum. Retroviruses 19:625-629 (2003).							
DR	HSSP; P12488; IM7;							
DR	GO; GO:0016021; C:integral to membrane; IEA.							
DR	GO; GO:0019028; C:viral capsid; IEA.							
DR	GO; GO:0019031; C:viral envelope; IEA.							
DR	GO; GO:0005198; P:structural molecule activity; IEA.							
DR	InterPro; IPR00328; Env_GP41.							
DR	PFam; PF00517; GP41; 1.							
KW	Coat protein; Envelope protein; Glycoprotein; Transmembrane.							
FT	NON_TER 1							
SQ	SEQUENCE 122 AA; 14763 MW; B9227B0EBEB4213AA CRC64;							
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3	1 RILAEVRYLKDQQLGIGWGSCKLIC 26							
Db	19 RILAEVRYLKDQQLGIGWGSCKLIC 44							
RESULT 9								
Q9QIU3	PRELIMINARY;	PRT;	122 AA.					
AC								
DT	01-MAY-2000 (TREMBLrel. 13, Created)							
DT	01-JUN-2003 (TREMBLrel. 24, Last annotation update)							
Q9QIU3	Query Match 100.0%; Best Local Similarity 100.0%; Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
Q9QIU3								

Db	17 RILAVERTYLKDQQLGIGWCGSKLIC 42	FT	NON TER	144	144 AA;	16907 MW;	A427C02C24218BEB CRC64;
RESULT 13							
Q698W3	PRELIMINARY;	PRT;	134 AA.		Query Match	100 0%;	Score 139; DB 2; Length 144;
ID					Best Local Similarity	100 0%;	Pred. No. 2.3e-13;
AC	Q698W3_				Matches	26;	Conservative 0; Mismatches 0;
DT	25-OCT-2004 (TREMBLrel. 28, Created)				Indels	0	Gaps 0;
DT	25-OCT-2004 (TREMBLrel. 28, Last sequence update)						
DE	Envelope glycoprotein (Fragment)						
GN	Name=env;						
OS	Human immunodeficiency virus 1.						
OC	Viruses; Retroviridae; Lentivirus.						
NCBI_TAXID=11676;							
OX							
RN	[1]						
RP	SEQUENCE FROM N.A.						
RA	Ndemb N., Takehisa J., Zekeng L., Kobayashi E., Ngansop C.,						
RA	Songok M.E., Takemura T., Ido E., Hayami M., Kaputu L., Ichimura H.;						
RA	"Emergence of New Forms of HIV type 1 in Cameroon, West-Central Africa.",						
RT	Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.						
RL	EMBL; AY541023; AAT0343..;						
DR	GO; GO:0005198; F: structural molecule activity; IEA.						
DR	GO:0005198; F: viral envelope; IEA.						
DR	InterPro; IPR000328; Env_GP41.						
DR	PFam; PF00517; GP41; 1.						
DR	Coat protein; Envelope protein; Glycoprotein; Transmembrane.						
DR	GO; GO:0019031; C:viral envelope; IEA.						
DR	Staub T., Boule R., Arendt V., Schneider F., Hemmer R., Schmit J.-C.;						
DR	"Uncommon mutations at residue positions critical for enfuvirtide (T-20) resistance in envirovirenaive patients infected with subtype B and non-B HIV-1 strains."						
DR	J. Acquir. Immune Defic. Syndr. 33:134-139 (2003).						
DR	EMBL; AY185383; AA065658..1; -.						
DR	HSSP; P04578; 1AIK.						
DR	GO; GO:0016021; C:integral to membrane; IEA.						
DR	GO; GO:0019028; C:viral capsid; IEA.						
DR	GO; GO:0019031; C:viral envelope; IEA.						
DR	GO; GO:0005198; F:structural molecule activity; IEA.						
DR	InterPro; IPR000328; Env_GP41.						
DR	Pfam; PF00517; GP41; 1.						
DR	Coat protein; Envelope protein; Glycoprotein; Transmembrane.						
DR	KW						
FT	NON_TER	134 AA;	A33CAA85195F8FDB	CRC64;	FT	NON_TER	1 1
FT	SEQUENCE	134 AA;	16199 MW;		FT	NON_TER	144 144
FT	Query Match	100 0%;	Score 139; DB 2;	Length 134;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100.0%;	Pred. No. 2.1e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 134;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100.0%;	Pred. No. 2.1e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
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FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
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FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
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FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
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FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
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FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
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FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
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FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
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FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
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FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 139; DB 2;	Length 144;	FT	SEQUENCE	144 AA;
FT	Best Local Similarity	100 0%;	Pred. No. 2.3e-13;		FT	SEQUENCE	144 AA;
FT	Matches	26;	Conservative 0; Mismatches 0;	Indels 0;	FT	SEQUENCE	144 AA;
FT	NON_TER	1			FT	SEQUENCE	144 AA;
FT	NON_TER	134			FT	SEQUENCE	144 AA;
FT	SEQUENCE	134 AA;	16199 MW;		FT	SEQUENCE	144 AA;
FT	Query Match	100 0%;	Score 1				

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4 protein - protein search, using sw model

Run on: March 3, 2005, 17:13:03 ; Search time 39 Seconds
(without alignments)
64.145 Million cell updates/sec

Title: US-09-733-239-1

Perfect score: 139

Sequence: 1 RILAVERYLKDDQQLLIGCGSGKLIC 26

Scoring table: BIOSTIME2

searched: 283416 seqs, 96216763 residues
 overall number of hits satisfying chosen parameters: 283416

maximum DB seq length: 0
maximum DB seq length: 2000000000

post-processing: Minimum Match 0% Maximum Match 100% ListArc First 45 summaries

database : PIR^{79;*}
1: pi1;* AIDS Res. Hum. Retroviruses 8, 53-59, 1992
ATitle: Distinct populations of human immunodeficiency virus type 1 in blood
AReference number: S70417; PMID: 9244209; PMID:1736940
AReference:

A) Accession: S70422
A) Status: Preliminary
A) Molecule type: DNA
A) Residues: 1-357 <ST2>
2: pir2:*3: pir3:*4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULTS

No.	Score	Match	Length	DB	ID	Description		Matches	26 ; Conservative	0 ; Mismatches	0 ; Indels	0 ; Gaps
						envelope	protein					
1	139	100.0	357	2	S21995							
2	139	100.0	358	2	S21995	envelope	protein					

				Db	80 RILAVERYLKDQQLG1WGCSKLLIC 105
3	12.9	100.0	853	2	S54384
4	12.9	100.0	854	2	S13288
5	12.9	100.0	855	1	VCLJZR

envelope protein gp120/gp41 - human immunodeficiency virus type 1	
6	env polyprotein pr
7	env polyprotein pr
8	env polyprotein pr
9	env polyprotein q
	result 2
	S21998
	envelope protein gp120/gp41 - human immunodeficiency virus type 1
	envelope protein gp120/gp41 - human immunodeficiency virus type 1, HIV-1
	envelope protein gp120/gp41 - human immunodeficiency virus type 1, HIV-1

13.8 99.3 852 1 VLRD env polyprotein -
13.7 98.6 856 1 A44963 env polyprotein pr
13.5 97.1 357 2 S21990 envelope protein g
13.5 97.1 358 2 S20417 envelope protein g

20	135	97.1	143	2	A1621	env polyprotein D
21	135	97.1	454	2	B1621	env polyprotein D
22	135	97.1	843	2	H4001	env polyprotein D
23	135	97.1	852	2	T12016	env polyprotein D

C; Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 358;
Best Local Similarity 100.0%; Pred. No. 2.2e-13; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLIGWGSGKLIC 26
Db 81 RILAVERYLKDQQLIGWGSGKLIC 106

RESULT 3
S54304
env<polyprotein - human immunodeficiency virus type 1, HIV-1>
C; Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C; Accession: S54304
R; Theodore, T.; Buckler-White, A.J.
Submitted to the EMBL Data Library, July 1989
A; Reference number: S54304
A; Accession: S54304
A; Status: Preliminary
A; Molecule type: genomic RNA
A; Residues: 1-853 <THE>
A; Cross-references: UNIPROT:PI12487; EMBL:M22639; PMID:9329377; PIDN:AAA45370.1; PMID:93293
C; Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 853;
Best Local Similarity 100.0%; Pred. No. 5.4e-13; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLIGWGSGKLIC 26
Db 576 RILAVERYLKDQQLIGWGSGKLIC 601

RESULT 4
S12288
env<polyprotein - human immunodeficiency virus type 1, HIV-1>
C; Species: human immunodeficiency virus type 1, HIV-1
C; Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C; Accession: 113288
R; O'Brian, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A; Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A; Reference number: S13288; PMID:91043044; PMID:2172833
A; Accession: S13288
A; Status: Preliminary
A; Molecule type: DNA
A; Residues: 1-854 <OBRA>
C; Superfamily: type E retrovirus env polyprotein

Query Match 100.0%; Score 139; DB 2; Length 854;
Best Local Similarity 100.0%; Pred. No. 5.4e-13; Indels 0; Gaps 0;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLIGWGSGKLIC 26
Db 577 RILAVERYLKDQQLIGWGSGKLIC 602

RESULT 5
VCLJYV
env<polyprotein precursor - human immunodeficiency virus Zr-6>
N; Alternative names: coat polyprotein
C; Species: human immunodeficiency virus Zr-6
C; Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C; Accession: D26192
R; Srinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Peotino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A; Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleoti

A; Reference number: A26192; MUID:87248097; PMID:3036660
A; Accession: D26192
A; Molecule type: DNA
A; Residues: 1-855 <SR1>
C; Cross-references: UNIPROT:PO4580; GB:K03458; PIDN:AAA45380.1; I
C; Genet:

A; Gene: env
C; Superfamily: type E retrovirus env polyprotein
C; Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyproto

F; 1-19 Domain: signal sequence #status predicted <SIG>
F; 20-855/Product: env polyprotein #status predicted <SIG>
F; 501-550/Product: exterior membrane glycoprotein #status predicted <TMM>
F; 87,129,140-145,154,158,186,189,199,236,243,264,278,291,297,333,340-355,386,392,398,404,
Query Match 100.0%; Score 139; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLIGWGSGKLIC 26
Db 578 RILAVERYLKDQQLIGWGSGKLIC 603

RESULT 6
VCLJH3
env<polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)>
N; Alternative names: coat polyprotein
C; Species: human immunodeficiency virus type 1, HIV-1
A; Note: host Homo sapiens (man)
C; Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C; Accession: A03973
R; Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Josephs, S.F.; Doran
berger, J.A.; Papas, T.S.; Grayeb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
A; Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A; Reference number: A93353; MUID:85111123; PMID:2578615
A; Accession: A03973
A; Molecule type: DNA
A; Residues: 1-856 <DAT>
A; Cross-references: UNIPROT:PO3375; GB:K02009; GB:K02010; NID:9326;
C; Genet:

A; Gene: env
C; Superfamily: type E retrovirus env polyprotein
C; Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyproto

F; 1-30 Domain: signal sequence #status predicted <SIG>
F; 31-511/Product: exterior membrane glycoprotein #status predicted <TMM>
F; 512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F; 88,136,141,156,160,186,197,230,234,241,262,276,289,295,301,312,339,356,386,392,397,406,
F; 611,616,625,637,674,750,816 Binding site: carbohydrate (Asn) (Covalent) #status predict

Query Match 100.0%; Score 139; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 5.4e-13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RILAVERYLKDQQLIGWGSGKLIC 26
Db 579 RILAVERYLKDQQLIGWGSGKLIC 604

RESULT 7
VCLJYV
env<polyprotein precursor - human immunodeficiency virus type 1 (isolate LV)>
N; Alternative names: coat polyprotein
C; Species: human immunodeficiency virus type 1, HIV-1
A; Note: host Homo sapiens (man)
C; Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 09-Jul-2004
C; Accession: A03974
R; Muesig, M.A.; Smith, D.H.; Cabradilla, C.D.; Benton, C.V.; Lasky, L.A.; Capon, D.J.
Nature 313, 450-456, 1985
A; Title: Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovi
A; Reference number: A93355; MUID:85111157; PMID:2982104
A; Accession: A03974

A;Molecule type: DNA
 A;Residues: 1-856 <MUB>
 A;Cross-references: UNIPROT:PO3376; GB:K02083; NID:9555008; PIDN:AAB59873.1; PMID:9328559
 C;Genetics:
 A;Gene: env
 C;Superfamily: type B retrovirus env polyprotein
 C;Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprotein
 P;1-30/Domain: signal sequence #status predicted <SIG>
 P;31-51/Product: exterior membrane glycoprotein #status Predicted <EXT>
 P;52-856/Product: transmembrane glycoprotein #status Predicted <TMM>
 P;88-136,141,156,160,186,197,210,234,241,262,276,289,301,332,339,356,386,392,397,406
 P;611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status Predicted
 Qy 1 RILAYERYLKDQQLGIGWCGSKLIC 26
 Best Local Similarity 100.0%; Score 139; DB 1; Length 856;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 579 RILAYERYLKDQQLGIGWCGSKLIC 604

RESULT 10
 S22006
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 4L)
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 A;Accession: S70420; S22006
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebroc
 A;Reference number: S70417; MUID:92144209; PMID:1736940
 A;Accession: S70420
 A;Molecule type: DNA
 A;Residues: 1-357 <ST2>
 A;Cross-references: UNIPROT:Q78156; EMBL:X61354; NID:960190; PIDN:CAA43620.1; PMID:960191
 A;Experimental source: patient L
 A;Note: submitted to the EMBL Data Library, July 1991
 C;Superfamily: type E retrovirus env polyprotein

Query Match 99.3%; Score 138; DB 2; Length 357;
 Best Local Similarity 96.2%; Pred. No. 3.1e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RILAYERYLKDQQLGIGWCGSKLIC 26
 Db 80 RILAYERYLKDQQLGIGWCGSKLIC 105

RESULT 11
 S21992
 envelope protein gp120/gp41 - human immunodeficiency virus type 1 (patient 22)
 C;Species: human immunodeficiency virus type 1, HIV-1
 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
 A;Accession: S70424; S21992
 R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.
 AIDS Res. Hum. Retroviruses 8, 53-59, 1992
 A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebroc
 A;Reference number: S70417; MUID:92144209; PMID:1736940
 A;Accession: S70424
 A;Molecule type: DNA
 A;Residues: 1-357 <ST2>
 A;Cross-references: UNIPROT:Q78112; EMBL:X61358; NID:960177; PIDN:CAA43628.1; PMID:960178
 A;Experimental source: patient 22
 C;Superfamily: type E retrovirus env polyprotein

Query Match 99.3%; Score 138; DB 2; Length 357;
 Best Local Similarity 96.2%; Pred. No. 3.1e-13;
 Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RILAYERYLKDQQLGIGWCGSKLIC 26
 Db 80 RILAYERYLKDQQLGIGWCGSKLIC 105

RESULT 12

S2194 envelope protein gp120/gp41 - human immunodeficiency virus type 1, HIV-1

C;Species: human immunodeficiency virus type 1, HIV-1

A;Variety: isolate 27B

C;Accession: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.; Hacke, W.

A;Description: Submitted to the EMBL Data Library, July 1991

A;Reference number: S21940

A;Accession: S2194

A;Molecule type: DNA

A;Residues: 1-357 <STE1>

A;Cross-references: UNIPROT:Q78118; EMBL:X61355; NID:960179; PIDN:CAA43622.1; PID:960180

R;Steuler, H.; Storch-Hagenlocher, B.; Wildemann, B.

AIDS Res. Hum. Retroviruses 8, 53-59, 1992

A;Title: Distinct populations of human immunodeficiency virus type 1 in blood and cerebrospinal fluid as determined by the EMBL Data Library, July 1991

A;Reference number: S70417; MUID:92144209; PMID:1735940

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-140 'X' 142-312 'X' 314-357 <STE2>

A;Cross-references: EMBL:X61355; NID:960179

C;Superfamily: type E retrovirus env polyprotein

Query Match 99.3%; Score 138; DB 2; Length 357;

Best Local Similarity 96.2%; Pred. No. 3..e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 80 RLVAVERYLKDQQLGIGNGCSGKLLIC 105

RESULT 13

VCHJBR env polyprotein - human immunodeficiency virus type 1 (isolate BR)

N;Alternate names: coat polyprotein

N;Contains: coat protein gp120; coat protein gp41

C;Species: human immunodeficiency virus type 1, HIV-1

A;Note: host Homo sapiens (man)

C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004

R;Anand, R.; Thaver, R.; Srinivasan, A.; Nayyar, S.; Gardner, M.; Luciw, P.; Dandekar, S.

Virology 168: 79-89, 1989

A;Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1)

A;Reference number: A94389; MUID:89085613; PMID:2799516

A;Accession: A31167

A;Molecule type: DNA

A;Residues: 1-852 <ANA>

A;Cross-references: UNIPROT:PI12488

C;Keywords: type E retrovirus env polyprotein

C;Keywords: capsid protein; coat protein; polyprotein; transmembrane protein

F;1-516/Product: coat protein gp120 #status predicted <CP1>

F;517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match 99.3%; Score 138; DB 1; Length 852;

Best Local Similarity 96.2%; Pred. No. 7..e-13;

Matches 25; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RLVAVERYLKDQQLGIGNGCSGKLLIC 26

Db 575 RLVAVERYLKDQQLGIGNGCSGKLLIC 600

RESULT 14

A44963 env polyprotein precursor - human immunodeficiency virus type 1 (isolate 2321)

N;Alternate names: coat polyprotein

N;Contains: coat protein gp120; coat protein gp41